

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

| | | |
|----------------|---|---|
| Applicant | : | Dutron et al. |
| Appl. No. | : | 10/527,387 |
| Filed | : | October 17, 2005 |
| For | : | USE OF FAMILY 8 ENZYMES WITH XYLANOLYTIC ACTIVITY IN BAKING |
| Examiner | : | Badr, Hamid R. |
| Group Art Unit | : | 1794 |

DECLARATION UNDER 37 C.F.R. §1.132

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Dear Sir:

I, Thierry Dauvrin, declare and state:

1. I am Senior Research Manager at Puratos, N.V., the assignee of the above-referenced patent application, and am an inventor on the above-referenced patent application.
2. I am an expert in the field of enzymatic enhancement of bakery products. I have been head of the Research & Development Department of the Business Unit "Enzymes" of the Puratos Group for more than 10 years.
3. I am an inventor of 6 patents, have authored about 10 peer reviewed scientific papers and have given oral presentations at about 6 scientific meetings.
4. I am familiar with the above-referenced application, pending claims and current Office Action. I understand that the claims were rejected as allegedly being obvious over Fuglsang et al. (WO 02/19828 "R1"), in view of Collins et al. (J. Biol. Chem. 277:35133-35139,

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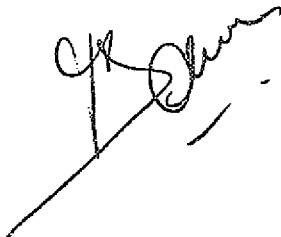
2002 "R2"), Olesen et al. (US 6,110,508) and JP 2001-245665 (machine translation). I have reviewed the pending claims and these references.

5. This Declaration is being submitted to demonstrate that the xylanase from *Bacillus halodurans* disclosed by JP 2001-245665 is not a family 8 enzyme. I performed a BLAST analysis of the amino acid sequence of the *B. halodurans* xylanase described in JP 2001-245665. The results, which are shown in Exhibit A, demonstrate that this enzyme exhibits 100 % sequence identity to another xylanase from *B. halodurans* and to a xylanase from *Bacillus firmus*, and 86 % sequence identity to a xylanase from *Paenibacillus* sp. DG-22, which are all three family 11 xylanases. From this analysis, I conclude that the xylanase disclosed in JP 2001-245665 is a family 11 xylanase, and is not a family 8 xylanase.

6. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information or belief are believed to be true, and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful statements may jeopardize the validity of the application or any patent issued thereon.

By: Thierry DAUVRIN


Date: 2009/08/12



7623662
081109

BLAST Basic Local Alignment Search Tool

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Bacillus halodurans xylanase JP2001 245 665Results for: [lcl|3017](#) None(210aa) 

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID

lcl|3017

Description

None

Molecule type

amino acid

Query Length

210

Database Name

nr

Description

All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects

ProgramBLASTP 2.2.21+ [Citation](#)**Reference**

Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Reference - compositional score matrix adjustment

Stephen F. Altschul, John C. Wootton, E. Michael Gertz, Richa Agarwala, Aleksandr Morgulis, Alejandro A. Schäffer, and Yi-Kuo Yu (2005) "Protein database searches using compositionally adjusted substitution matrices", FEBS J. 272:5101-5109.

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#) [Multiple alignment](#) [NEW](#)**Search Parameters**

| | |
|-------------------------|----------|
| Program | blastp |
| Word size | 3 |
| Expect value | 10 |
| Hittist size | 10 |
| Gapcosts | 11,1 |
| Matrix | BLOSUM62 |
| Threshold | 11 |
| Composition-based stats | 2 |
| Filter string | F |
| Genetic Code | 1 |
| Window Size | 40 |

Database

| | |
|---------------------|----------------------|
| Posted date | Aug 11, 2009 5:42 PM |
| Number of letters | 3,244,132,065 |
| Number of sequences | 9,489,734 |
| Entrez query | none |

Karlin-Altschul statistics

| Params | Ungapped | Gapped |
|--------|----------|--------|
| Lambda | 0.316054 | 0.267 |
| K | 0.131596 | 0.041 |
| H | 0.434666 | 0.14 |

Results Statistics

| | |
|------------------------------|--------------|
| Length adjustment | 130 |
| Effective length of query | 80 |
| Effective length of database | 2010409162 |
| Effective search space | 160832732960 |
| Effective search space used | 160832732960 |

Graphic Summary**Show Conserved Domains**

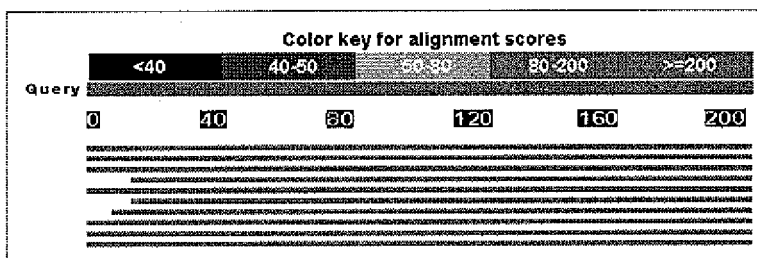
Putative conserved domains have been detected, click on the image below for detailed results.

**Distribution of 10 Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a

hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Descriptions

| Sequences producing significant alignments: | Score (Bits) | E Value |
|--|-----------------|-----------------|
| [ref NP_241765.1] endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125] | 423 | 6e-117 G |
| [gb BA04618.1] xylanase 11A [Bacillus firmus] | 422 | 1e-116 |
| [gb AA012276.1] xylanase A [Paenibacillus sp. DG-22] | 345 | 2e-93 |
| [ref ZP_04852431.1] endo-beta-1,4-xylanase [Paenibacillus sp. oral taxon 786 str.] | 344 | 4e-93 |
| [gb AB066887.1] endo-xylanase [Paenibacillus sp. HY8] | 342 | 1e-92 |
| [ref F45705.2] XANA BACFE RecName: Full=Endo-1,4-beta-xylanase A... | 338 | 2e-91 |
| [ref ZP_03059729.1] Endo-1,4-beta-xylanase [Geobacillus sp. Y4...] | 333 | 5e-90 |
| [gb BA083579.1] beta-1,4-xylanase [Paenibacillus sp. W-61] >d... | 327 | 5e-88 |
| [ref YP_003013454.1] Endo-1,4-beta-xylanase [Paenibacillus sp. ...] | 327 | 6e-88 G |
| [gb BA04618.1] xylanase I precursor [Aeromonas punctata] | 326 | 8e-88 |

Alignments [Select All](#) [Get selected sequences](#) [Distance tree of results](#) [Multiple alignment](#) **NEW**>ref|NP_241765.1| **G** endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]dbj|BA04618.1| **G** endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]

gb|AA012276.1| endo-1,4-beta-xylanhydrolase [Bacillus halodurans]

gb|AAQ14588.1| xylanase [Bacillus firmus]

Length=210

GENE ID: 893828 BH0899 | endo-1,4-beta-xylanhydrolase
[Bacillus halodurans C-125] (Over 10 PubMed links)Score = 423 bits (1087), Expect = 6e-117, Method: Compositional matrix adjust.
Identities = 210/210 (100%), Positives = 210/210 (100%), Gaps = 0/210 (0%)Query 1 MFKEVTKVLTVVIAATISFCLSAVPASANTYQYWTGCGGTVNATNGPGGNYSVTWRTDG 60
Sbjct 1 MFKEVTKVLTVVIAATISFCLSAVPASANTYQYWTGCGGTVNATNGPGGNYSVTWRTDG 60Query 61 NFVVGKGWEIGSPNRTIHYNAGVWEPSCNGYLTLYGWTNRNQLIEYYVVDNWGTYRPTGTH 120
Sbjct 61 NFVVGKGWEIGSPNRTIHYNAGVWEPSCNGYLTLYGWTNRNQLIEYYVVDNWGTYRPTGTH 120Query 121 RGTVVSDDGGTYDIYTTMRYNAPSIDGTQTFQCFWSVRQSKRPTGNNVSIITFSNHVNAWRN 180
Sbjct 121 RGTVVSDDGGTYDIYTTMRYNAPSIDGTQTFQCFWSVRQSKRPTGNNVSIITFSNHVNAWRN 180Query 181 AGMNLGSSWSYQVLATEGYQSSGRSNVTW 210
Sbjct 181 AGMNLGSSWSYQVLATEGYQSSGRSNVTW 210>gb|AAQ83579.1| xylanase 11A [Bacillus firmus]
Length=210Score = 422 bits (1085), Expect = 1e-116, Method: Compositional matrix adjust.
Identities = 209/210 (99%), Positives = 210/210 (100%), Gaps = 0/210 (0%)Query 1 MFKEVTKVLTVVIAATISFCLSAVPASANTYQYWTGCGGTVNATNGPGGNYSVTWRTDG 60
Sbjct 1 MFKEVTKVLTVVIAATISFCLSAVPASANTYQYWTGCGGTVNATNGPGGNYSVTWRTDG 60Query 61 NFVVGKGWEIGSPNRTIHYNAGVWEPSCNGYLTLYGWTNRNQLIEYYVVDNWGTYRPTGTH 120
Sbjct 61 NFVVGKGWEIGSPNRTIHYNAGVWEPSCNGYLTLYGWTNRNQLIEYYVVDNWGTYRPTGTH 120Query 121 RGTVVSDDGGTYDIYTTMRYNAPSIDGTQTFQCFWSVRQSKRPTGNNVSIITFSNHVNAWRN 180
Sbjct 121 RGTVVSDDGGTYDIYTTMRYNAPSIDGTQTFQCFWSVRQSKRPTGNNVSIITFSNHVNAWRN 180Query 181 AGMNLGSSWSYQVLATEGYQSSGRSNVTW 210
Sbjct 181 AGMNLGSSWSYQVLATEGYQSSGRSNVTW 210>gb|AB196991.1| xylanase A [Paenibacillus sp. DG-22]
Length=211Score = 345 bits (884), Expect = 2e-93, Method: Compositional matrix adjust.
Identities = 173/211 (81%), Positives = 186/211 (88%), Gaps = 1/211 (0%)Query 1 MFKEVTKVLTVVIAATISFCLSAVPASANT-YWQYWTGCGGTVNATNGPGGNYSVTWRTD 59
Sbjct 1 M K K LTV IAA +SF L A ++A T YWQYWTGCGGTVNATNGPGGNYSVTW + 60Query 60 GNFVVGKGWEIGSPNRTIHYNAGVWEPSCNGYLTLYGWTNRNQLIEYYVVDNWGTYRPTGT 119
Sbjct 61 GNFVVGKGW GSP RT++YNAGVW PSENGYLTLYGWTNRN LIEYYVVD+WGTYRPTGT 120Query 120 HRCITVVSDDGGTYDIYTTMRYNAPSIDGTQTFQCFWSVRQSKRPTGNNVSIITFSNHVNAWR 179
Sbjct 121 ++GTV SDGGTYDIYTTMRYNAPSIDGTQTF Q+WSVRQSKRPTG+NVSITFSNHVNAWR 180Query 180 NAGMNLGSSWSYQVLATEGYQSSGRSNVTW 210
Sbjct 181 NAGMNLGSSW+YQVLA EGYQSSG +NVTW 211

>ref|ZP_04852431.1| endo-beta-1,4-xylanase [Paenibacillus sp. oral taxon 786 str.]

gb|EES73557.1| endo-beta-1,4-xylanase [Paenibacillus sp. oral taxon 786 str.]
Length=210Score = 344 bits (882), Expect = 4e-93, Method: Compositional matrix adjust.
Identities = 171/197 (86%), Positives = 184/197 (93%), Gaps = 1/197 (0%)Query 15 ATISFCLSAVPASANT-YWQYWTGCGGTVNATNGPGGNYSVTWRTDGNFVVGKGWEIGSP 73
Sbjct 14 A++SF L ++SA T YWQYWTGCGGTVN NG GGNYSVTW+++GNFVVGKGW +GSP 73Query 74 NRTIHYNAGVWEPSCNGYLTLYGWTNRNQLIEYYVVDNWGTYRPTGTHRGTVVSDDGGTYDI 133
Sbjct 74 NRTIHYNAGVWEPSCNGYLTLYGWTNRN LIEYYVVD+WGTYRPTGTH+GTV SDGGTYDI 133Query 134 YTTMRYNAPSIDGTQTFQCFWSVRQSKRPTGNNVSIITFSNHVNAWRNAGMNLGSSWSYQV 193
Sbjct 134 YTTMRYNAPSIDGTQTFQCFWSVRQSKRPTG+NVSITFSNHVNAWR+ GMNLGSSWSYQV 193

Sbjct 134 YTTMRYNAPSIDGTQTFQFWSVRQSKRPTGSSNVSIITFSNHVNAWRSGMNLGSSWSYQV 193
 Query 194 LATEGYQSSGRSNVTVM 210
 LATEGYQSSGRSNVTVM
 Sbjct 194 LATEGYQSSGRSNVTVM 210

>gb|ABD66557.1| endo-xylanase [Paenibacillus sp. HY8]
 Length=211

Score = 342 bits (877), Expect = 1e-92, Method: Compositional matrix adjust.
 Identities = 171/211 (81%), Positives = 187/211 (88%), Gaps = 1/211 (0%)

Query 1 MFKEFVKVLTIVVIAATISFCLSAVPASANT-YWQYWTGSGGTVNATNGPGGNYSVTWRTDT 59
 MFKEF K+LTVV+AA++SF + A +SA T YWQ WTDGGGTVNA NG GGNYSVTW++T
 Sbjct 1 MFKEFSKKMLTIVLAASMSFGVFAATSSAATDYQWQNTDGGGTVNAVNGSGGNYSVTWQNT 60
 Query 60 GNFVVGKGWEIGSPNRTIHYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGT 119
 GNFVVGKGW +GSPNRTI+YNAGVW PSNGYLTLYGWTRN LIEYYVVD+WGTYRPTGT
 Sbjct 61 GNFVVGKGWNVGSPNRTIHYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGT 120
 Query 120 HRGTVVSDDGGTYDIYTTMRYNAPSIDGTQTFQFWSVRQSKRPTGNNVSIITFSNHVNAWR 179
 +GTV SDGGTYDIYTTMRYNAPSIDGTQTF Q+WSVRQSKR TG N +I FSNHVNWA
 Sbjct 121 FKGTVNSDDGGTYDIYTTMRYNAPSIDGTQTFQYWSVRQSKRATGVNSAIAFNSHVNAWA 180
 Query 180 NAGMNLGSSWSYQVLATEGYQSSGRSNVTVM 210
 + GMNLGSSWSYQVLATEGYQSSG SNVTVM
 Sbjct 181 SKGMNLGSSWSYQVLATEGYQSSGSSNVTVM 211

>sp|P45705.2|XYNA BACST RecName: Full=Endo-1,4-beta-xylanase A; Short=Xylanase A; AltName:
 Full=1,4-beta-D-xylan xylanohydrolase A; Flags: Precursor
 gb|AAB72117.1| endo-beta-1,4-xylanase [Geobacillus stearothermophilus]
 Length=210

Score = 338 bits (867), Expect = 2e-91, Method: Compositional matrix adjust.
 Identities = 168/197 (85%), Positives = 182/197 (92%), Gaps = 1/197 (0%)

Query 15 ATISFCLSAVPASANT-YWQYWTGSGGTVNATNGPGGNYSVTWRTDTGNFVVGKGWEIGSP 73
 A++SF L +SA T YWQYWTGSGG VNA NGPGGNYSVTW++TGNFVVGKGW +GSP
 Sbjct 14 ASMSFGLFEGATSSAATDYWQYWTGSGGMVNAVNGPGGNYSVTWQNTGNFVVGKGWTVGSP 73
 Query 74 NRTIHYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGTHRGTVVSDDGGTYDI 133
 NR I+YNAG+WEPSPGNGYLTLYGWTRN LIEYYVVD+WGTYRPTG ++GTV SDGGTYDI
 Sbjct 74 NRVIYNAGIWEPSGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGNYKGTVNSDDGGTYDI 133
 Query 134 YTTMRYNAPSIDGTQTFQFWSVRQSKRPTGNNVSIITFSNHVNAWRNAGMNLGSSWSYQV 193
 YTTMRYNAPSIDGTQTFQFWSVRQSKRPTG+NVSIITFSNHVNAWR+ GMNLGSSW+YQV
 Sbjct 134 YTTMRYNAPSIDGTQTFQFWSVRQSKRPTGSSNVSIITFSNHVNAWRSGMNLGSSWAYQV 193
 Query 194 LATEGYQSSGRSNVTVM 210
 LATEGYQSSGRSNVTVM
 Sbjct 194 LATEGYQSSGRSNVTVM 210

>ref|ZP_03039720.1| Endo-1,4-beta-xylanase [Geobacillus sp. Y412MC10]
 gb|EDV76913.1| Endo-1,4-beta-xylanase [Geobacillus sp. Y412MC10]
 Length=203



Score = 333 bits (855), Expect = 5e-90, Method: Compositional matrix adjust.
 Identities = 168/203 (82%), Positives = 182/203 (89%), Gaps = 1/203 (0%)

Query 9 LTVVIAATISFCLSAVPASANT-YWQYWTGSGGTVNATNGPGGNYSVTWRTDTGNFVVGKG 67
 +T+V+AA++SF L A ++A T YWQ WTDGGGTVNA NG GGNYSVTW++TGNFVVGKG
 Sbjct 1 MTLVLAASMSFGLFATTSNAATDYQWQNTDGGGTVNAVNGSGGNYSVTWQNTGNFVVGKG 60
 Query 68 WEIGSPNRTIHYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGTHRGTVVSD 127
 W GSPNRTI+YNAGVW PSNGYLTLYGWTRN LIEYYVVD+WGTYRPTGTH+GTV SD
 Sbjct 61 WNTGSPNRTIHYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGTHRGTVVSD 120
 Query 128 GGTYYDIYTTMRYNAPSIDGTQTFQFWSVRQSKRPTGNNVSIITFSNHVNAWRNAGMNLG 187
 GGTYYDIYTTMRYNAPSIDGTQTF Q+WSVRQSKR TG N SITFSNHVNWA + GMNLG
 Sbjct 121 GGTYYDIYTTMRYNAPSIDGTQTFQYWSVRQSKRATGVNSITFSNHVNWAASKGMNLG 180
 Query 188 SWSYQVLATEGYQSSGRSNVTVM 210
 SWSYQVLATEGYQSSG SNVTVM
 Sbjct 181 SWSYQVLATEGYQSSGSSNVTVM 203

>dbj|BAE93061.1| beta-1,4-xylanase [Paenibacillus sp. W-61]
 dbj|BAF49080.1| Xylanase I [Paenibacillus sp. W-61]
 Length=211

Score = 327 bits (838), Expect = 5e-88, Method: Compositional matrix adjust.
 Identities = 164/211 (77%), Positives = 184/211 (87%), Gaps = 1/211 (0%)

Query 1 MFKEFVKVLTIVVIAATISFCLSAVPASANT-YWQYWTGSGGTVNATNGPGGNYSVTWRTDT 59
 MFKEF K+LTVV+AA++SF + A +SA T YWQ WTDGGGTVNA NG GGNYSV W++T
 Sbjct 1 MFKEFSKKMLTIVLAASMSFGVFAATSSAATDYQWQNTDGGGTVNAVNGSGGNYSVTWQNT 60
 Query 60 GNFVVGKGWEIGSPNRTIHYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGT 119
 GNFVVGKGW G+PNR ++YNAGV+ PSNGYLT YGWTRN LIEYYVVDNWGTYRPTGT
 Sbjct 61 GNFVVGKGWTYGTPNRVYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGT 120
 Query 120 HRGTVVSDDGGTYDIYTTMRYNAPSIDGTQTFQFWSVRQSKRPTGNNVSIITFSNHVNAWR 179
 ++GTV SDGGTYDIYTTMRYNAPSIDGTQTF Q+WSVRQ+KRP G N +ITFSNHVNWA
 Sbjct 121 YKGTVNSDDGGTYDIYTTMRYNAPSIDGTQTFQYWSVRQTKRPIGVNSTITFSNHVNWA 180
 Query 180 NAGMNLGSSWSYQVLATEGYQSSGRSNVTVM 210
 + GM LG+SWSYQV+ATEGYQSSG SNVTVM
 Sbjct 181 SKGMYLGNSWSYQVMATEGYQSSGSSNVTVM 211

>ref|YP_003013364.1|  Endo-1,4-beta-xylanase [Paenibacillus sp. JDR-2]
 gb|ACT03278.1|  Endo-1,4-beta-xylanase [Paenibacillus sp. JDR-2]
 Length=211

GENE ID: 8125650 Pjdr2_4664 | Endo-1,4-beta-xylanase [Paenibacillus sp. JDR-2]
 Score = 327 bits (837), Expect = 6e-88, Method: Compositional matrix adjust.
 Identities = 163/211 (77%), Positives = 180/211 (85%), Gaps = 1/211 (0%)

Query 1 MFKEFVKVLTIVVIAATISFCLSAVPASANT-YWQYWTGSGGTVNATNGPGGNYSVTWRTDT 59
 MEK KV+T V+AA++S L A A+T YWQ WTDGGGTVNA NG GGNYSV W +T
 Sbjct 1 MFKLKKVMTAVLAASMSIGLFAATANAATDYQWQNTDGGGTVNAVNGSGGNYSVTWQNT 60
 Query 60 GNFVVGKGWEIGSPNRTIHYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGT 119
 GNFVVGKGW GS +R I+YNAGVW PSNGYLTLYGWTRN LIEYYVVD+WGTYRPTGT
 Sbjct 61 GNFVVGKGWNTGASRVINYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNWGTYRPTGT 120

```

Query 120 HRGTVVSDGGTYDIYTTMRYNAPSIDGTQTFQQFWSVRQSKRPTGNNVSIITFSNHVNAWR 179
++GTV SDGGTYDIYT R NAPSIDGT TF Q+WSVRQSKR TG+NV+ITF+NHVNAW+
Sbjct 121 YKGTVSSDGGTYDIYTAQRVNAPSIDGTATFTQYWSVRQSKRATGSNVAITFANHVNNAWK 180

Query 180 NAGMNLGSSWSYQVLATEGYQSSGSRSNVTVM 210
+ GMNLGSSWSYQVLATEGYQSSG SNVTVM
Sbjct 181 SKGMNLGSSWSYQVLATEGYQSSGSSNVTVM 211

```

>dbj|BAA06837.1| xylanase I precursor [Aeromonas punctata]
Length=211

Score = 326 bits (836), Expect = 8e-88, Method: Compositional matrix adjust.
Identities = 163/211 (77%), Positives = 186/211 (88%), Gaps = 1/211 (0%)

```

Query 1 MEKEVTKVLTVVIAATISFCLSAVPASANT-YWQYWTIDGGGTVNATNGPGGNYSVTNRDT 59
MEKE K++TVV+AA++SF + A +SA T YWQ WTDGGGTVNA NG GGNYSV+W++T
Sbjct 1 MFKEGKKLMTVLAASMSFGVFAATSSAATDYQNWIDGGGTVNAVNGSGGNYSVSWQNT 60



Query 60 GNFFVVGKWEIGSPNRTIHYNAGVWEPSPGNGYLTLYGWTRNQLIEYYVVDNMGTYRPTGT 119
GNFFVVGKGW G+PNR ++YNAGV+ PSGNGYLT YGWTRN LIEYYVVD+NGTYRPTGT
Sbjct 61 GNFFVVGKWTYGTGNRVVNYNAGVTFAPSGNGYLTIFYGWTRNALIEYYVVDNMGTYRPTGT 120

Query 120 HRGTVVSDGGTYDIYTTMRYNAPSIDGTQTFQQFWSVRQSKRPTGNNVSIITFSNHVNAWR 179
++GTV SDGGTYDIYTTMRYNAPSIDGTQTF Q+WSVRQSKRPTG N +ITFSNHVNAW
Sbjct 121 YKGTVNSDGGTYDIYTTMRYNAPSIDGTQTFPQYWSVRQSKRPTGVNSTITFSNHVNAWP 180

Query 180 NAGMNLGSSWSYQVLATEGYQSSGSRSNVTVM 210
+ GM LG+SWSYQV+ATEGYQSSG +NVTVM
Sbjct 181 SKGMYLGNSWSYQVMATEGYQSSGNANVTVM 211

```

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[Structure](#)
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NCBI Reference Sequence: NP_241765.1

endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125][Comment](#) [Features](#) [Sequence](#)

LOCUS NP_241765 210 aa linear BCT 26-APR-2009
 DEFINITION endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125].
 ACCESSION NP_241765
 VERSION NP_241765.1 GI:15613462
 DBLINK Project:235
 DBSOURCE REFSEQ: accession NC_002570.2
 KEYWORDS
 SOURCE Bacillus halodurans C-125
 ORGANISM *Bacillus halodurans* C-125
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 REFERENCE 1 (residues 1 to 210)
 AUTHORS Takami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N., Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and Horikoshi,K.
 TITLE Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis
 JOURNAL Nucleic Acids Res. 28 (21), 4317-4331 (2000)
 PUBMED 11058132
 REFERENCE 2 (residues 1 to 210)
 AUTHORS Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T., Hirama,C., Fuji,F. and Takami,H.
 TITLE Characterization and comparative study of the rrn operons of alkaliphilic Bacillus halodurans C-125
 JOURNAL Extremophiles 4 (4), 209-214 (2000)
 PUBMED 10972182
 REFERENCE 3 (sites)
 AUTHORS Takami,H. and Horikoshi,K.
 TITLE Analysis of the genome of an alkaliphilic Bacillus strain from an industrial point of view
 JOURNAL Extremophiles 4 (2), 99-108 (2000)
 PUBMED 10605861
 REFERENCE 4 (sites)
 AUTHORS Takami,H., Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G., Sasaki,R., Hirama,C., Fuji,F. and Masui,N.
 TITLE Genetic analysis of the chromosome of alkaliphilic Bacillus halodurans C-125
 JOURNAL Extremophiles 3 (3), 227-233 (1999)
 PUBMED 10484179
 REFERENCE 5 (sites)
 AUTHORS Takami,H., Masui,N., Nakasone,K. and Horikoshi,K.
 TITLE Replication origin region of the chromosome of alkaliphilic Bacillus halodurans C-125
 JOURNAL Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
 PUBMED 10427704
 REFERENCE 6 (sites)
 AUTHORS Takami,H., Takaki,Y., Nakasone,K., Hirama,C., Inoue,A. and Horikoshi,K.
 TITLE Sequence analysis of a 32-kb region including the major ribosomal protein gene clusters from alkaliphilic Bacillus sp. strain C-125
 JOURNAL Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
 PUBMED 10129228
 REFERENCE 7 (sites)
 AUTHORS Takami,H., Nakasone,K., Ogasawara,N., Hirama,C., Nakamura,Y., Masui,N., Fuji,F., Takaki,Y., Inoue,A. and Horikoshi,K.
 TITLE Sequencing of three lambda clones from the genome of alkaliphilic Bacillus sp. strain C-125
 JOURNAL Extremophiles 3 (1), 29-34 (1999)
 PUBMED 10086842
 REFERENCE 8 (sites)
 AUTHORS Takami,H., Nakasone,K., Hirama,C., Takaki,Y., Masui,N., Fuji,F., Nakamura,Y. and Inoue,A.
 TITLE An improved physical and genetic map of the genome of alkaliphilic Bacillus sp. C-125
 JOURNAL Extremophiles 3 (1), 21-28 (1999)
 PUBMED 10086841
 REFERENCE 9 (sites)
 AUTHORS Takami,H.
 TITLE Genome analysis of facultatively alkaliphilic Bacillus halodurans C-125

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- ▶ BLAST Sequence
- ▶ Conserved Domains

Articles about the BH0899 gene

- ▶ Revision of the taxonomic position of the xylanolytic B. [Extremophiles. 2002]
- ▶ Cloning and characterization of two [Biochem Biophys Res Commun. 2004]
- ▶ Complete genome sequence of the alkaliphilic b. [Nucleic Acids Res. 2000]

» See all...


Identical Proteins for NP_241765.1

- ▶ unnamed protein product [E [CAJ29866] halodurans]
- ▶ xylanase [Bacillus firmus] [AAQ14588]
- ▶ endo-1,4-beta-xylanhydrolase [AAO12276] halodurans]





» See all...

More about the gene BH0899


Also Known As: BH0899

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-  xylanase Y [Bacillus halodurans]
-  bacillus halodurans xylan... (36)
-  endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]
-  **Protein Sequence (210 let...)** [BLAST](#)

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- ▶ Conserved Domains
- ▶ Full text in PMC
- ▶ Gene
- ▶ Genome Project
- ▶ Identical Proteins
- ▶ Nucleotide
- ▶ Protein Clusters
- ▶ PubMed (RefSeq)
- ▶ PubMed (Weighted)
- ▶ Related Structure
- ▶ Related Sequences

JOURNAL (in) Extremophiles in deep-sea environments (Ed.);
 . HORIKOSHI, K. TSUJII;
 : 249-284; Springer-Verlag (1999)
 REFERENCE 10 (sites)
 AUTHORS Takami, H. and Horikoshi, K.
 TITLE Reidentification of facultatively alkaliphilic *Bacillus* sp. C-125
 JOURNAL Biosci. Biotechnol. Biochem. 63, 943-945 (1999)
 REFERENCE 11 (residues 1 to 210)
 CONSRTM NCBI Genome Project
 TITLE Direct Submission
 JOURNAL Submitted (13-SEP-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 12 (residues 1 to 210)
 CONSRTM NCBI Microbial Genomes Annotation Project
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
 REFERENCE 13 (residues 1 to 210)
 AUTHORS Takami, H. and Takaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAR-2000) Japan Marine Science and Technology Center,
 Deep-sea Microorganisms Research Group, 2-15 Natsushima,
 Yokosuka,
 Kanagawa 237-0061, Japan
 COMMENT PROVISIONAL ~~REFSEQ~~: This record has not yet been subject to
 final

► Domain Relatives
 ► Genome
 ► PubMed
 ► Taxonomy
 ► LinkOut

NCBI review. The reference sequence was derived from [BAB04618](#).

FEATURES
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 121 rgtvvsdggd ydiyttmryn apsidgtqtf qqfwsvrqsk rptgnnvsit fshvnawrn
 181 agmnlgswws yqvlategyq ssgrsnvtvw
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GenBank: AAQ14588.1

xylanase [Bacillus firmus][Features](#) [Sequence](#)

LOCUS AAQ14588 210 aa linear BCT 01-NOV-2003

DEFINITION xylanase [Bacillus firmus].

ACCESSION AAQ14588

VERSION AAQ14588.1 GI:34451649

DBSOURCE accession AF317713.1

KEYWORDS

SOURCE Bacillus firmus

ORGANISM [Bacillus firmus](#)

REFERENCE 1 (residues 1 to 210)

AUTHORS Chuensumran,U., Ratanakhanokchai,K. and Cheevadhanarak,S.

TITLE Direct Submission

JOURNAL Submitted (29-OCT-2000) Pilot Plant Development and Training Institute, King Mongkut's University of Technology Thonburi, Prachauthit, Tungku, Bangkok 10140, Thailand

COMMENT Method: conceptual translation.

FEATURES

source Location/Qualifiers

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Sequence Analysis Tools

- ▶ BLAST Sequence
- ▶ Conserved Domains






Identical Proteins for AAQ14588.1

- ▶ unnamed protein product [E[CAJ29668] halodurans]
- ▶ endo-1,4-beta-xylanhydrol; [AAO12276] halodurans]
- ▶ endo-1,4-beta-xylanhydro [NP_241765] halodurans C-125]

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-  xylanase [Bacillus firmus]
-  xylanase Y [Bacillus halodurans]
-  [bacillus halodurans xylan...](#) (36)
-  endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]
-  [Protein Sequence \(210 let...](#) BLAST

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- ▶ Nucleotide
- ▶ PubMed (Weighted)
- ▶ Related Structure
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- ▶ Taxonomy
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GenBank: ABI96991.1

xylanase A [Paenibacillus sp. DG-22][Features](#) [Sequence](#)

LOCUS ABI96991 211 aa linear BCT 12-MAR-2007
 DEFINITION xylanase A [Paenibacillus sp. DG-22].
 ACCESSION ABI96991
 VERSION ABI96991.1 GI:115394008
 DBSOURCE accession [DQ869568.1](#)
 KEYWORDS
 SOURCE Paenibacillus sp. DG-22
 ORGANISM [Paenibacillus sp. DG-22](#)
 Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.
 REFERENCE 1 (residues 1 to 211)
 AUTHORS Lee,T.H., Lim,P.O. and Lee,Y.E.
 TITLE Cloning, characterization, and expression of xylanase A gene from Paenibacillus sp. DG-22 in Escherichia coli
 JOURNAL J. Microbiol. Biotechnol. 17 (1), 29-36 (2007)
 PUBMED [18051350](#)
 REFERENCE 2 (residues 1 to 211)
 AUTHORS Lee,T.H., Lim,P.O. and Lee,Y.-E.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUL-2006) Biotechnology, Dongguk University, Sukjang-Dong 707, Kyungju, Kyongbuk 780-714, Korea
 COMMENT Method: conceptual translation supplied by author.
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 181 nagmnlgsaw ayqvlavegy qssgsanvtv w
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Identical Proteins for ABI96991.1

- ▶ [Sequence 1 from patent U:\[AAC84548\]](#)

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-  xylanase A [Paenibacillus sp. DG-22]
-  xylanase [Bacillus firmus]
-  xylanase Y [Bacillus halodurans]
-  [bacillus halodurans xylan...](#) (36) Protein
-  endo-1,4-beta-xylanhydrolase [Bacillus halodurans C-125]

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